

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5           (i) APPLICANT:                   ANDREW C. HIATT, JULIAN  
  K.-C. MA, THOMAS LEHNER

          (ii) TITLE OF INVENTION:       IMMUNOGLOBULINS CONTAINING PROTECTION  
  PROTEINS IN PLANTS AND THEIR USES

10          (iii) NUMBER OF SEQUENCES:     19

          (iv) CORRESPONDENCE ADDRESS:

15           (A) ADDRESSEE:               Lyon & Lyon  
              (B) STREET:                633 West Fifth Street  
  Suite 4700  
              (C) CITY:                  Los Angeles  
              (D) STATE:                 California  
20           (E) COUNTRY:                U.S.A.  
              (F) ZIP:                  90071

          (v) COMPUTER READABLE FORM:

25           (A) MEDIUM TYPE:            3.5" Diskette, 1.44 Mb  
  storage  
              (B) COMPUTER:              IBM Compatible  
              (C) OPERATING SYSTEM:     IBM P.C. DOS 5.0  
              (D) SOFTWARE:             Word Perfect 5.1

30          (vi) CURRENT APPLICATION DATA:

          (A) APPLICATION NUMBER:       TO BE ASSIGNED  
          (B) FILING DATE:  
35           (C) CLASSIFICATION:

          (vii) PRIOR APPLICATION DATA:

          Prior applications total,  
40           including application  
          described below:             1

          U.S. Patent Application Serial No. 08/367,395  
          Filed 12/30/94  
45           Docket No. 210/152

## (viii) ATTORNEY/AGENT INFORMATION:

5 (A) NAME: Guise, Jeffr y W.  
(B) REGISTRATION NUMBER: 34,613  
(C) REFERENCE/DOCKET NUMBER: 212/127

## (ix) TELECOMMUNICATION INFORMATION:

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2025 RELEASE

## SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 3517 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

15 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 124....2445

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCCGGGGTT ACGGGCTGGC CAGCAGGCTG TGCCCCGAG TCCGGTCAGCAGGAGGGGAA 60  
 GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA 120  
 25 GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG 168  
 Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala  
 1 5 10 15  
 30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC 216  
 Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro  
 20 25 30  
 35 GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC 264  
 Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr  
 35 40 45  
 40 TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG 312  
 Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg  
 50 55 60  
 45 GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG 360  
 Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr  
 65 70 75  
 TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA 408  
 Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys  
 80 85 90 95  
 50 GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG 456  
 Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly  
 100 105 110  
 55 AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT 504  
 Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly  
 115 120 125  
 GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC 552  
 Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr  
 130 135 140  
 60 AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT 600  
 Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr  
 145 150 155  
 65 GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA 648

	Ala	Thr	Arg	Gln	Leu	Lys	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu	
	160					165					170					175	
5	CTT	GTA	CTC	ATC	ATT	GAT	TCC	AGC	AGT	AAG	GAG	GCA	AAG	GAC	CCC	AGG	696
	Leu	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg	
					180					185					190		
10	TAT	AAG	GGC	AGA	ATA	ACG	TTG	CAG	ATC	CAA	AGT	ACC	ACA	GCA	AAA	GAA	744
	Tyr	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu	
				195					200					205			
15	TTC	ACA	GTC	ACC	ATC	AAG	CAT	TTG	CAG	CTC	AAT	GAT	GCT	GGG	CAG	TAT	792
	Phe	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	
			210					215					220				
20	GTC	TGC	CAG	AGT	GGA	AGC	GAC	CCC	ACT	GCT	GAA	GAA	CAG	AAC	GTT	GAC	840
	Val	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	
		225					230					235					
25	CTC	CGA	CTG	CTA	ACT	CCT	GGT	CTG	CTC	TAT	GGA	AAC	CTG	GGG	GGC	TCG	888
	Leu	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	
						245					250					255	
30	GTG	ACC	TTT	GAA	TGT	GCC	CTG	GAC	TCT	GAA	GAC	GCA	AAC	GCG	GTA	GCA	936
	Val	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	
					260					265					270		
35	TCC	TTG	CGC	CAG	GTT	AGG	GGT	GGC	AAT	GTG	GTC	ATT	GAC	AGC	CAG	GGG	984
	Ser	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	
				275					280					285			
40	ACA	ATA	GAT	CCA	GCC	TTC	GAG	GGC	AGG	ATC	CTG	TTC	ACC	AAG	GCT	GAG	1032
	Thr	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	
			290					295					300				
45	AAC	GGC	CAC	TTC	AGT	GTA	GTG	ATC	GCA	GGC	CTG	AGG	AAG	GAA	GAC	ACA	1080
	Asn	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	
		305					310					315					
50	GGG	AAC	TAT	CTG	TGC	GGA	GTC	CAG	TCC	AAT	GGT	CAG	TCT	GGG	GAT	GGG	1128
	Gly	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	
		320				325					330					335	
55	CCC	ACC	CAG	CTT	CGG	CAA	CTC	TTC	GTC	AAT	GAA	GAG	ATC	GAC	GTG	TCC	1176
	Pro	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	
					340					345					350		
60	CGC	AGC	CCC	CCT	GTG	TTG	AAG	GGC	TTT	CCA	GGA	GGC	TCC	GTG	ACC	ATA	1224
	Arg	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	
				355					360					365			
65	CGC	TGC	CCC	TAC	AAC	CCG	AAG	AGA	AGC	GAC	AGC	CAC	CTG	CAG	CTG	TAT	1272
	Arg	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	
			370					375					380				
70	CTC	TGG	GAA	GGG	AGT	CAA	ACC	CGC	CAT	CTG	CTG	GTG	GAC	AGC	GGC	GAG	1320
	Leu	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	
		385					390					395					
75	GGG	CTG	GTT	CAG	AAA	GAC	TAC	ACA	GGC	AGG	CTG	GCC	CTG	TTC	GAA	GAG	1368
	Gly	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	
		400				405					410					415	
80	CCT	GGC	AAT	GGC	ACC	TTC	TCA	GTC	GTC	CTC	AAC	CAG	CTC	ACT	GCC	GAG	1416
	Pro	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	
					420					425						430	

	GAT	GAA	GGC	TTC	TAC	TGG	TGT	GTC	AGC	GAT	GAC	GAT	GAG	TCC	CTG	ACG	1464
	Asp	Glu	Gly	Phe	Tyr	Trp	Cys	Val	Ser	Asp	Asp	Asp	Glu	Ser	Leu	Thr	
				435					440					445			
5	ACT	TCG	GTG	AAG	CTC	CAG	ATC	GTT	GAC	GGA	GAA	CCA	AGC	CCC	ACG	ATC	1512
	Thr	Ser	Val	Lys	Leu	Gln	Ile	Val	Asp	Gly	Glu	Pro	Ser	Pro	Thr	Ile	
				450				455						460			
10	GAC	AAG	TTC	ACT	GCT	GTG	CAG	GGA	GAG	CCT	GTT	GAG	ATC	ACC	TGC	CAC	1560
	Asp	Lys	Phe	Thr	Ala	Val	Gln	Gly	Glu	Pro	Val	Glu	Ile	Thr	Cys	His	
				465			470						475				
15	TTC	CCA	TGC	AAA	TAC	TTC	TCC	TCC	GAG	AAG	TAC	TGG	TGC	AAG	TGG	AAT	1608
	Phe	Pro	Cys	Lys	Tyr	Phe	Ser	Ser	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	
				480		485						490				495	
20	GAC	CAT	GGC	TGC	GAG	GAC	CTG	CCC	ACT	AAG	CTC	AGC	TCC	AGC	GGC	GAC	1656
	Asp	His	Gly	Cys	Glu	Asp	Leu	Pro	Thr	Lys	Leu	Ser	Ser	Ser	Gly	Asp	
					500					505					510		
25	CTT	GTG	AAA	TGC	AAC	AAC	AAC	CTG	GTC	CTC	ACC	CTG	ACC	TTG	GAC	TCG	1704
	Leu	Val	Lys	Cys	Asn	Asn	Asn	Leu	Val	Leu	Thr	Leu	Thr	Leu	Asp	Ser	
				515					520					525			
30	GTC	AGC	GAA	GAT	GAC	GAG	GGC	TGG	TAC	TGG	TGT	GGC	GCG	AAA	GAC	GGG	1752
	Val	Ser	Glu	Asp	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Ala	Lys	Asp	Gly	
				530				535						540			
35	CAC	GAG	TTT	GAA	GAG	GTT	GCG	GCC	GTC	AGG	GTG	GAG	CTG	ACA	GAG	CCA	1800
	His	Glu	Phe	Glu	Glu	Val	Ala	Ala	Val	Arg	Val	Glu	Leu	Thr	Glu	Pro	
				545			550						555				
40	GCC	AAG	GTA	GCT	GTC	GAG	CCA	GCC	AAG	GTA	CCT	GTC	GAC	CCA	GCC	AAG	1848
	Ala	Lys	Val	Ala	Val	Glu	Pro	Ala	Lys	Val	Pro	Val	Asp	Pro	Ala	Lys	
						565					570					575	
45	GCA	GCC	CCC	GCG	CCT	GCT	GAG	GAG	AAG	GCC	AAG	GCG	CGG	TGC	CCA	GTG	1896
	Ala	Ala	Pro	Ala	Pro	Ala	Glu	Glu	Lys	Ala	Lys	Ala	Arg	Cys	Pro	Val	
					580					585					590		
50	CCC	AGG	AGA	AGG	CAG	TGG	TAC	CCA	TTG	TCA	AGG	AAG	CTG	AGA	ACA	AGT	1944
	Pro	Arg	Arg	Arg	Gln	Trp	Tyr	Pro	Leu	Ser	Arg	Lys	Leu	Arg	Thr	Ser	
					595				600					605			
55	TGT	CCA	GAA	CCT	CGG	CTC	CTT	GCG	GAG	GAG	GTA	GCA	GTG	CAG	AGT	GCG	1992
	Cys	Pro	Glu	Pro	Arg	Leu	Leu	Ala	Glu	Glu	Val	Ala	Val	Gln	Ser	Ala	
				610				615						620			
60	GAA	GAC	CCA	GCC	AGT	GGG	AGC	AGA	GCG	TCT	GTG	GAT	GCC	AGC	AGT	GCT	2040
	Glu	Asp	Pro	Ala	Ser	Gly	Ser	Arg	Ala	Ser	Val	Asp	Ala	Ser	Ser	Ala	
				625			630					635					
65	TCG	GGA	CAA	AGC	GGG	AGT	GCC	AAA	GTA	CTG	ATC	TCC	ACC	CTG	GTG	CCC	2088
	Ser	Gly	Gln	Ser	Gly	Ser	Ala	Lys	Val	Leu	Ile	Ser	Thr	Leu	Val	Pro	
						645					650					655	
70	TTG	GGG	CTG	GTG	CTG	GCA	GCG	GGG	GCC	ATG	GCC	GTG	GCC	ATA	GCC	AGA	2136
	Leu	Gly	Leu	Val	Leu	Ala	Ala	Gly	Ala	Met	Ala	Val	Ala	Ile	Ala	Arg	
					660				665						670		
75	GCC	CGG	CAC	AGG	AGG	AAC	GTG	GAC	CGA	GTT	TCC	ATC	GGA	AGC	TAC	AGG	2184
	Ala	Arg	His	Arg	Arg	Asn	Val	Asp	Arg	Val	Ser	Ile	Gly	Ser	Tyr	Arg	
				675				680						685			
80	ACA	GAC	ATT	AGC	ATG	TCA	GAC	TTG	GAG	AAC	TCC	AGG	GAG	TTC	GGA	GCC	2232
	Thr	Asp	Ile	Ser	Met	Ser	Asp	Leu	Glu	Asn	Ser	Arg	Glu	Phe	Gly	Ala	

	690	695	700	
5	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GCC CTC GGA Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly 705 710 715			2280
10	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu 720 725 730 735			2328
15	GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala 740 745 750			2376
20	TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln 755 760 765			2424
25	GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC Asp Gly Pro Lys Glu Ala 770			2480
30	CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAATCACGT TGATCCTCGG GGTCCCCAGA GCCGGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT GCCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCATCCAGG CCTGGCTCAA TGTTCCTGTT GGGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCCGTTTC TCCCGAGAGA AGCTAAGGAT CCAGGTCCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT TGATGAGGAG GCCAGAGGCG CTTTCCGGCC ACCCCCTCCC TCCCTGCCCC CACCTCCTT CCTTCATTCA AAAGTCCCAG TGGTGCTGTC CTAGGGTCCA GGCCTGGGCC GCACGCCTCC TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC TCACTCAGGC ATCCTGTCTT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG CCCTGGGCGT GTCTGCAAGT CACCCAGAC ACATGTTCTC GCCATTTTAC AGATGAGAAC ACTGAGGTTG TACTCAAGG CACCTGCGA GATGGAGCAA CAGCAAATA GATGGGCTTC TGCTGTCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCCT GCCCCTGTAG GAAGCAGAGT TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC ACGGGGGAAA AGGCCCCCTC CTTTTCTGTC ACTCTCGGGG ACCTGCGGAG TTGAGCATTC GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGGTC CTTGTCCCTG TGAGCTTTAA CCAGCACCTC CGGGCTGACC CTTGCTAACA CATCAGAAAT GTGATTAAAT CATTAAACAT TGTGATTGCC ACTGGGA			2540 2600 2660 2720 2780 2840 2900 2960 3020 3080 3140 3200 3260 3320 3380 3440 3500 3517

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 amino acids

TCCTTCTGTT

(B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala Ala  
 1 5 10 15  
 10 Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly  
 20 25 30  
 15 Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr  
 35 40 45  
 Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu  
 50 55 60  
 20 Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser  
 65 70 75 80  
 Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly  
 85 90 95  
 25 Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser  
 100 105 110  
 Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly Val  
 115 120 125  
 Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr Lys  
 130 135 140  
 35 Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala  
 145 150 155 160  
 Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu  
 165 170 175  
 40 Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr  
 180 185 190  
 Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe  
 195 200 205  
 Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val  
 210 215 220  
 50 Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp Leu  
 225 230 235 240  
 Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser Val  
 245 250 255  
 55 Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala Ser  
 260 265 270  
 Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly Thr  
 275 280 285  
 60 Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu Asn  
 290 295 300  
 Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr Gly  
 305 310 315 320

	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	Pro
					325					330					335	
5	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	Arg
				340					345					350		
	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	Arg
			355					360					365			
10	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	Leu
		370					375					380				
	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	Gly
	385					390					395					400
15	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	Pro
					405					410					415	
20	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	Asp
				420					425					430		
	Glu	Gly	Phe	Tyr	Trp	Cys	Val	Ser	Asp	Asp	Asp	Glu	Ser	Leu	Thr	Thr
			435					440					445			
25	Ser	Val	Lys	Leu	Gln	Ile	Val	Asp	Gly	Glu	Pro	Ser	Pro	Thr	Ile	Asp
		450					455					460				
	Lys	Phe	Thr	Ala	Val	Gln	Gly	Glu	Pro	Val	Glu	Ile	Thr	Cys	His	Phe
	465					470					475					480
30	Pro	Cys	Lys	Tyr	Phe	Ser	Ser	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	Asp
					485					490					495	
	His	Gly	Cys	Glu	Asp	Leu	Pro	Thr	Lys	Leu	Ser	Ser	Ser	Gly	Asp	Leu
				500					505					510		
35	Val	Lys	Cys	Asn	Asn	Asn	Leu	Val	Leu	Thr	Leu	Thr	Leu	Asp	Ser	Val
			515					520					525			
40	Ser	Glu	Asp	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Ala	Lys	Asp	Gly	His
		530					535					540				
	Glu	Phe	Glu	Glu	Val	Ala	Ala	Val	Arg	Val	Glu	Leu	Thr	Glu	Pro	Ala
	545					550					555					560
45	Lys	Val	Ala	Val	Glu	Pro	Ala	Lys	Val	Pro	Val	Asp	Pro	Ala	Lys	Ala
					565					570					575	
	Ala	Pro	Ala	Pro	Ala	Glu	Glu	Lys	Ala	Lys	Ala	Arg	Cys	Pro	Val	Pro
				580					585					590		
50	Arg	Arg	Arg	Gln	Trp	Tyr	Pro	Leu	Ser	Arg	Lys	Leu	Arg	Thr	Ser	Cys
			595					600					605			
55	Pro	Glu	Pro	Arg	Leu	Leu	Ala	Glu	Glu	Val	Ala	Val	Gln	Ser	Ala	Glu
		610					615					620				
	Asp	Pro	Ala	Ser	Gly	Ser	Arg	Ala	Ser	Val	Asp	Ala	Ser	Ser	Ala	Ser
	625					630					635					640
60	Gly	Gln	Ser	G												



Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg Thr  
 675 680 685

5 Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala Ile  
 690 695 700

Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly Gly  
 705 710 715 720

10 Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu Glu  
 725 730 735

Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala Tyr  
 740 745 750

15 Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln Asp  
 755 760 765

20 Gly Pro Lys Glu Ala  
 770

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2919 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Human polyimmunoglobulin Receptor

35 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 235....2472

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG 60

GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG 120

45 GCTAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA 180

ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACG AAG 237  
 Lys  
 1

50 AGT CCC ATA TTT GGT CCC GAG GAG GTG AAT AGT GTG GAA GGT AAC TCA 285  
 Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn Ser  
 5 10 15

55 GTG TCC ATC ACG TGC TAC TAC CCA CCC ACC TCT GTC AAC CGG CAC ACC 333  
 Val Ser Ile Thr Cys Tyr Tyr Pro Thr Ser Val Asn Arg His Thr  
 20 25 30

60 CGG AAG TAC TGG TGC CGG CAG GGA GCT AGA GGT GGC TGC ATA ACC CTC 381  
 Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr Leu  
 35 40 45

65 ATC TCC TCG GAG GGC TAC GTC TCC AGC AAA TAT GCA GGC AGG GCT AAC 429  
 Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala Asn  
 50 55 60 65

	CTC ACC AAC TTC CCG GAG AAC GGC ACA TTT GTG GTG AAC ATT GCC CAG	477
	Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala Gln	
	70 75 80	
5	CTG AGC CAG GAT GAC TCC GGG CGC TAC AAG TGT GGC CTG GGC ATC AAT	525
	Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Asn	
	85 90 95	
10	AGC CGA GGC CTG TCC TTT GAT GTC AGC CTG GAG GTC AGC CAG GGT CCT	573
	Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly Pro	
	100 105 110	
15	GGG CTC CTA AAT GAC ACT AAA GTC TAC ACA GTG GAC CTG GGC AGA ACG	621
	Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg Thr	
	115 120 125	
20	GTG ACC ATC AAC TGC CCT TTC AAG ACT GAG AAT GCT CAA AAG AGG AAG	669
	Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg Lys	
	130 135 140 145	
25	TCC TTG TAC AAG CAG ATA GGC CTG TAC CCT GTG CTG GTC ATC GAC TCC	717
	Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp Ser	
	150 155 160	
30	AGT GGT TAT GTG AAT CCC AAC TAT ACA GGA AGA ATA CGC CTT GAT ATT	765
	Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp Ile	
	165 170 175	
35	CAG GGT ACT GGC CAG TTA CTG TTC AGC GTT GTG ATC AAC CAA CTC AGG	813
	Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu Arg	
	180 185 190	
40	CTC AGC GAT GCT GGG CAG TAT CTC TGC CAG GCT GGG GAT GAT TCC AAT	861
	Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser Asn	
	195 200 205	
45	AGT AAT AAG AAG AAT GCT GAC CTC CAA GTG CTA AAG CCC GAG CCC GAG	909
	Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro Glu	
	210 215 220 225	
50	CTG GTT TAT GAA GAC CTG AGG GGC TCA GTG ACC TTC CAC TGT GCC CTG	957
	Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala Leu	
	230 235 240	
55	GGC CCT GAG GTG GCA AAC GTG GCC AAA TTT CTG TGC CGA CAG AGC AGT	1005
	Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser Ser	
	245 250 255	
60	GGG GAA AAC TGT GAC GTG GTC GTC AAC ACC CTG GGG AAG AGG GCC CCA	1053
	Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala Pro	
	260 265 270	
65	GCC TTT GAG GGC AGG ATC CTG CTC AAC CCC CAG GAC AAG GAT GGC TCA	1101
	Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly Ser	
	275 280 285	
70	TTC AGT GTG GTG ATC ACA GGC CTG AGG AAG GAG GAT GCA GGG CGC TAC	1149
	Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg Tyr	
	290 295 300 305	
75	CTG TGT GGA GCC CAT TCG GAT GGT CAG CTG CAG GAA GGC TCG CCT ATC	1197
	Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro Ile	
	310 315 320	
80	CAG GCC TGG CAA CTC TTC GTC AAT GAG GAG TCC ACG ATT CCC CGC AGC	1245
	Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg Ser	

	325										330										335										
5	CCC Pro	ACT Thr	GTG Val	GTG Val	AAG Lys	GGG Gly	GTG Val	GCA Ala	GGA Gly	AGC Ser	TCT Ser	GTG Val	GCC Ala	GTG Val	CTC Leu	TGC Cys	1293														
	340				345				350																						
10	CCC Pro	TAC Tyr	AAC Asn	CGT Arg	AAG Lys	GAA Glu	AGC Ser	AAA Lys	AGC Ser	ATC Ile	AAG Lys	TAC Tyr	TGG Trp	TGT Cys	CTC Leu	TGG Trp	1341														
	355				360				365																						
15	GAA Glu	GGG Gly	GCC Ala	CAG Gln	AAT Asn	GGC Gly	CGC Arg	TGC Cys	CCC Pro	CTG Leu	CTG Leu	GTG Val	GAC Asp	AGC Ser	GAG Glu	GGG Gly	1389														
	370				375				380				385																		
20	TGG Trp	GTT Val	AAG Lys	GCC Ala	CAG Gln	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	CTC Leu	TCC Ser	CTG Leu	CTG Leu	GAG Glu	GAG Glu	CCA Pro	1437														
	390				395				400																						
25	GGC Gly	AAC Asn	GGC Gly	ACC Thr	TTC Phe	ACT Thr	GTC Val	ATC Ile	CTC Leu	AAC Asn	CAG Gln	CTC Leu	ACC Thr	AGC Ser	CGG Arg	GAC Asp	1485														
	405				410				415																						
30	GCC Ala	GGC Gly	TTC Phe	TAC Tyr	TGG Trp	TGT Cys	CTG Leu	ACC Thr	AAC Asn	GGC Gly	GAT Asp	ACT Thr	CTC Leu	TGG Trp	AGG Arg	ACC Thr	1533														
	420				425				430																						
35	ACC Thr	GTG Val	GAG Glu	ATC Ile	AAG Lys	ATT Ile	ATC Ile	GAA Glu	GGA Gly	GAA Glu	CCA Pro	AAC Asn	CTC Leu	AAG Lys	GTA Val	CCA Pro	1581														
	435				440				445																						
40	GGG Gly	AAT Asn	GTC Val	ACG Thr	GCT Ala	GTG Val	CTG Leu	GGA Gly	GAG Glu	ACT Thr	CTC Leu	AAG Lys	GTC Val	CCC Pro	TGT Cys	CAC His	1629														
	450				455				460																						
45	TTT Phe	CCA Pro	TGC Cys	AAA Lys	TTC Phe	TCC Ser	TCG Ser	TAC Tyr	GAG Glu	AAA Lys	TAC Tyr	TGG Trp	TGC Cys	AAG Lys	TGG Trp	AAT Asn	1677														
	470				475				480																						
50	AAC Asn	ACG Thr	GGC Gly	TGC Cys	CAG Gln	GCC Ala	CTG Leu	CCC Pro	AGC Ser	CAA Gln	GAC Asp	GAA Glu	GGC Gly	CCC Pro	AGC Ser	AAG Lys	1725														
	485				490				495																						
55	GCC Ala	TTC Phe	GTG Val	AAC Asn	TGT Cys	GAC Asp	GAG Glu	AAC Asn	AGC Ser	CGG Arg	CTT Leu	GTC Val	TCC Ser	CTG Leu	ACC Thr	CTG Leu	1773														
	500				505				510																						
60	AAC Asn	CTG Leu	GTG Val	ACC Thr	AGG Arg	GCT Ala	GAT Asp	GAG Glu	GGC Gly	TGG Trp	TAC Tyr	TGG Trp	TGT Cys	GGA Gly	GTG Val	AAG Lys	1821														
	515				520				525																						
65	CAG Gln	GGC Gly	CAC His	TTC Phe	TAT Tyr	GGA Gly	GAG Glu	ACT Thr	GCA Ala	GCC Ala	GTC Val	TAT Tyr	GTG Val	GCA Ala	GTT Val	GAA Glu	1869														
	530				535				540																						
70	GAG Glu	AGG Arg	AAG Lys	GCA Ala	GCG Ala	GGG Gly	TCC Ser	CGC Arg	GAT Asp	GTC Val	AGC Ser	CTA Leu	GCG Ala	AAG Lys	GCA Ala	GAC Asp	1917														
	550				555				560																						
75	GCT Ala	GCT Ala	CCT Pro	GAT Asp	GAG Glu	AAG Lys	GTG Val	CTA Leu	GAC Asp	TCT Ser	GGT Gly	TTT Phe	CGG Arg	GAG Glu	ATT Ile	GAG Glu	1965														
	565				570				575																						
80	AAC Asn	AAA Lys	GCC Ala	ATT Ile	CAG Gln	GAT Asp	CCC Pro	AGG Arg	CTT Leu	TTT Phe	GCA Ala	GAG Glu	GAA Glu	AAG Lys	GCG Ala	GTG Val	2013														
	580				585				590																						

	GCA GAT ACA AGA GAT CAA GCC GAT GGG AGC AGA GCA TCT GTG GAT TCC Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp Ser 595 600 605	2061
5	GGC AGC TCT GAG GAA CAA GGT GGA AGC TCC AGA GCG CTG GTC TCC ACC Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg Ala Leu Val Ser Thr 610 615 620 625	2109
10	CTG GTG CCC CTG GGC CTG GTG CTG GCA GTG GGA GCC GTG GCT GTG GGG Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Gly 630 635 640	2157
15	GTG GCC AGA GCC CGG CAC AGG AAG AAC GTC GAC CGA GTT TCA ATC AGA Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile Arg 645 650 655	2205
20	AGC TAC AGG ACA GAC ATT AGC ATG TCA GAC TTC GAG AAC TCC AGG GAA Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Glu 660 665 670	2253
25	TTT GGA GCC AAT GAC AAC ATG GGA GCC TCT TCG ATC ACT CAG GAG ACA Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr 675 680 685	2301
30	TCC CTC GGA GGA AAA GAA GAG TTT GTT GCC ACC ACT GAG AGC ACC ACA Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr 690 695 700 705	2349
35	GAG ACC AAA GAA CCC AAG AAG GCA AAA AGG TCA TCC AAG GAG GAA GCC Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala 710 715 720	2397
40	GAG ATG GCC TAC AAA GAC TTC CTG CTC CAG TCC AGC ACC GTG GCC GCC Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala 725 730 735	2445
45	GAG GCC CAG GAC GGC CCC CAG GAA GCC TAGACGGTGT CGCCGCCTGC TCCCTGCA Glu Ala Gln Asp Gly Pro Gln Glu Ala 740 745	2500
50	CCCATGACAA TCACCTTCAG AATCATGTCG ATCCTGGGGG CCCTCAGCTC CTGGGGACCC CACTCCCTGC TCTAACACCT GCCTAGGTTT TTCCTACTGT CCTCAGAGGC GTGCTGGTCC CCTCCTCAGT GACATCAAAG CCTGGCCTAA TTGTTCTTAT TGGGGATGAG GGTGGCATGA GGAGGTCCCA CTGCAACTT CTTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG GTCCTCATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA GAGACGTGCA GCGCCCCCTCT GCACCCTTAT CATGGGATGT CAACAGAATT TTTCCCTCC ACTCCATCCC TCCCTCCCGT CCTTCCCCTC TTCTTCTTTC CTTACCATCA AAAGATGTA	2560 2620 2680 2740 2800 2860 2919

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Human Polyimmunoglobulin Receptor

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5 Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn  
 1 5 10 15  
 Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His  
 20 25 30  
 10 Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr  
 35 40 45  
 Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala  
 50 55 60  
 15 Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala  
 65 70 75 80  
 Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile  
 85 90 95  
 20 Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly  
 100 105 110  
 Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg  
 115 120 125  
 Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg  
 130 135 140  
 30 Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp  
 145 150 155 160  
 Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp  
 165 170 175  
 35 Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu  
 180 185 190  
 Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser  
 195 200 205  
 40 Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro  
 210 215 220  
 Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala  
 225 230 235 240  
 Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser  
 245 250 255  
 50 Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala  
 260 265 270  
 Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly  
 275 280 285  
 55 Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg  
 290 295 300  
 60 Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro  
 305 310 315 320  
 Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg  
 325 330 335  
 65 Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu

	340								345						350						
	Cys	Pro	Tyr	Asn	Arg	Lys	Glu	Ser	Lys	Ser	Ile	Lys	Tyr	Trp	Cys	Leu					
			355					360					365								
5	Trp	Glu	Gly	Ala	Gln	Asn	Gly	Arg	Cys	Pro	Leu	Leu	Val	Asp	Ser	Glu					
	370						375					380									
10	Gly	Trp	Val	Lys	Ala	Gln	Tyr	Glu	Gly	Arg	Leu	Ser	Leu	Leu	Glu	Glu					
	385					390					395				400						
	Pro	Gly	Asn	Gly	Thr	Phe	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr	Ser	Arg					
					405					410					415						
15	Asp	Ala	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asn	Gly	Asp	Thr	Leu	Trp	Arg					
				420					425					430							
	Thr	Thr	Val	Glu	Ile	Lys	Ile	Ile	Glu	Gly	Glu	Pro	Asn	Leu	Lys	Val					
			435					440					445								
20	Pro	Gly	Asn	Val	Thr	Ala	Val	Leu	Gly	Glu	Thr	Leu	Lys	Val	Pro	Cys					
	450						455					460									
25	His	Phe	Pro	Cys	Lys	Phe	Ser	Ser	Tyr	Glu	Lys	Tyr	Trp	Cys	Lys	Trp					
	465					470					475					480					
	Asn	Asn	Thr	Gly	Cys	Gln	Ala	Leu	Pro	Ser	Gln	Asp	Glu	Gly	Pro	Ser					
					485					490					495						
30	Lys	Ala	Phe	Val	Asn	Cys	Asp	Glu	Asn	Ser	Arg	Leu	Val	Ser	Leu	Thr					
				500					505					510							
	Leu	Asn	Leu	Val	Thr	Arg	Ala	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Val					
			515					520					525								
35	Lys	Gln	Gly	His	Phe	Tyr	Gly	Glu	Thr	Ala	Ala	Val	Tyr	Val	Ala	Val					
	530						535					540									
40	Glu	Glu	Arg	Lys	Ala	Ala	Gly	Ser	Arg	Asp	Val	Ser	Leu	Ala	Lys	Ala					
	545					550					555					560					
	Asp	Ala	Ala	Pro	Asp	Glu	Lys	Val	Leu	Asp	Ser	Gly	Phe	Arg	Glu	Ile					
					565					570					575						
45	Glu	Asn	Lys	Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	Glu	Lys	Ala					
				580					585					590							
	Val	Ala	Asp	Thr	Arg	Asp	Gln	Ala	Asp	Gly	Ser	Arg	Ala	Ser	Val	Asp					
			595					600					605								
50	Ser	Gly	Ser	Ser	Glu	Glu	Gln	Gly	Gly	Ser	Ser	Arg	Ala	Leu	Val	Ser					
	610						615					620									
55	Thr	Leu	Val	Pro	Leu	Gly	Leu	Val	Leu	Ala	Val	Gly	Ala	Val	Ala	Val					
	625					630					635					640					
	Gly	Val	Ala	Arg	Ala	Arg	His	Arg	Lys	Asn	Val	Asp	Arg	Val	Ser	Ile					
					645					650					655						
60	Arg	Ser	Tyr	Arg	Thr	Asp	Ile	Ser	Met	Ser	Asp	Phe	Glu	Asn							

690 695 700

Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu  
705 710 715 720

5 Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala  
725 730 735

10 Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala  
740 745

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3630 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
DESCRIPTION: Bovine Polyimmunoglobulin Receptor

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 152....2425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30 GATCTCCTCG GAGGGTCGTG CAGCGGCCCT GGGTCCCTGC CGGCACCACT ACTTGCGCGT 60

GTGCTCCCAA AGCTGACGGG ATAGGAGGAA GGAGCTCAAA CAACCACACA GGACGGTGGC 120

35 TGGCGGCAGA GACCCGCGGG AGCCCCCAGC G ATG TCG CGC CTG TTC CTC GCC 172  
Met Ser Arg Leu Phe Leu Ala  
1 5

40 TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC 220  
Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe  
10 15 20

45 GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG 268  
Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys  
25 30 35

50 TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG 316  
Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp  
40 45 50 55

55 TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG 364  
Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu  
60 65 70

60 CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA 460  
Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys  
90 95 100

65 GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT 508  
Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu  
105 110 115

	AAC TTC GAT GTG AGC CTG GAG GTC AGC CAA GAT CCT GCA CAG GCA AGT	556
	Asn Phe Asp Val Ser Leu Glu Val Ser Gln Asp Pro Ala Gln Ala Ser	
	120 125 130 135	
5	CAT GCC CAC GTC TAC ACT ATA GAC CTG GGC AGG ACT GTG ACC ATC AAC	604
	His Ala His Val Tyr Thr Ile Asp Leu Gly Arg Thr Val Thr Ile Asn	
	140 145 150	
10	TGC CCT TTC ACG CGT GCG AAT TCT GAG AAG AGA AAA TCC TTG TGC AAG	652
	Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys	
	155 160 165	
15	AAG ACA ATC CAG GAC TGT TTC CAA GTT GTC GAC TCC ACC GGG TAT GTG	700
	Lys Thr Ile Gln Asp Cys Phe Gln Val Val Asp Ser Thr Gly Tyr Val	
	170 175 180	
	AGC AAC AGC TAT AAA GAC AGA GCA CAT ATC AGT ATC CTA GGT ACC AAC	748
	Ser Asn Ser Tyr Lys Asp Arg Ala His Ile Ser Ile Leu Gly Thr Asn	
	185 190 195	
20	ACA TTA GTG TTC AGC GTT GTC ATC AAC CGA GTC AAG CTC AGT GAT GCT	796
	Thr Leu Val Phe Ser Val Val Ile Asn Arg Val Lys Leu Ser Asp Ala	
	200 205 210 215	
25	GGG ATG TAT GTC TGC CAG GCT GGG GAC GAT GCC AAA GCC GAT AAA ATC	844
	Gly Met Tyr Val Cys Gln Ala Gly Asp Asp Ala Lys Ala Asp Lys Ile	
	220 225 230	
30	AAC ATT GAC CTC CAG GTG CTG GAG CCT GAG CCT GAG CTG GTT TAT GGA	892
	Asn Ile Asp Leu Gln Val Leu Glu Pro Glu Pro Glu Leu Val Tyr Gly	
	235 240 245	
35	GAC TTG AGG AGC TCG GTG ACC TTT GAC TGT TCC CTG GGC CCC GAG GTG	940
	Asp Leu Arg Ser Ser Val Thr Phe Asp Cys Ser Leu Gly Pro Glu Val	
	250 255 260	
	GCA AAT GTG CCC AAA TTT CTG TGC CAG AAG AAG AAT GGG GGA GCT TGC	988
	Ala Asn Val Pro Lys Phe Leu Cys Gln Lys Lys Asn Gly Gly Ala Cys	
	265 270 275	
40	AAT GTA GTC ATC AAC ACG TTG GGG AAG AAG GCT CAG GAC TTC CAG GGC	1036
	Asn Val Val Ile Asn Thr Leu Gly Lys Lys Ala Gln Asp Phe Gln Gly	
	280 285 290 295	
45	AGG ATC GTG TCC GTG CCC AAG GAC AAT GGT GTC TTC AGT GTG CAC ATT	1084
	Arg Ile Val Ser Val Pro Lys Asp Asn Gly Val Phe Ser Val His Ile	
	300 305 310	
50	ACC AGC CTG AGG AAA GAG GAC GCA GGG CGC TAC GTG TGC GGG GCC CAG	1132
	Thr Ser Leu Arg Lys Glu Asp Ala Gly Arg Tyr Val Cys Gly Ala Gln	
	315 320 325	
55	CCT GAG GGT GAG CCC CAG GAC GGC TGG CCT GTG CAG GCC TGG CAA CTC	1180
	Pro Glu Gly Glu Pro Gln Asp Gly Trp Pro Val Gln Ala Trp Gln Leu	
	330 335 340	
	TTC GTC AAT GAA GAG ACG GCA ATC CCC GCA AGC CCC TCC GTG GTG AAA	1228
	Phe Val Asn Glu Glu Thr Ala Ile Pro Ala Ser Pro Ser Val Val Lys	
	345 350 355	
60	GGT GTG AGG GGA GGC TCT GTG ACT GTA TCT TGC CCC TAC AAC CCT AAG	1276
	Gly Val Arg Gly Gly Ser Val Thr Val Ser Cys Pro Tyr Asn Pro Lys	
	360 365 370 375	
65	GAT GCC AAC AGC GCG AAG TAC TGG TGT CAC TGG GAA GAG GCT CAA AAC	1324
	Asp Ala Asn Ser Ala Lys Tyr Trp Cys His Trp Glu Glu Ala Gln Asn	



	380	385	390	
5	GGC CGC TGC CCG CGG CTG GTG GAG AGC CGG GGG CTG ATG AAG GAG CAG Gly Arg Cys Pro Arg Leu Val Glu Ser Arg Gly Leu Met Lys Glu Gln 395 400 405			1372
10	TAC GAG GGC AGG CTG GTG CTG CTC ACC GAG CCG GGC AAC GGC ACC TAC Tyr Glu Gly Arg Leu Val Leu Leu Thr Glu Pro Gly Asn Gly Thr Tyr 410 415 420			1420
15	ACC GTC ATC CTC AAC CAG CTC ACC GAT CAG GAC GCC GGC TTC TAC TGG Thr Val Ile Leu Asn Gln Thr Thr Asp Gln Asp Ala Gly Phe Tyr Trp 425 430 435			1468
20	TGC GTG ACC GAC GGC GAC ACG CGC TGG ATC TCC ACA GTG GAG CTC AAG Cys Val Thr Asp Gly Asp Thr Arg Trp Ile Ser Thr Val Glu Leu Lys 440 445 450 455			1516
25	GTT GTC CAA GGA GAA CCA AGC CTC AAG GTA CCC AAG AAC GTC ACG GCT Val Val Gln Gly Glu Pro Ser Leu Lys Val Pro Lys Asn Val Thr Ala 460 465 470			1564
30	TGG CTG GGA GAG CCC TTA AAG CTC TCC TGC CAC TTC CCC TGC AAA TTC Trp Leu Gly Glu Pro Leu Lys Leu Ser Cys His Phe Pro Cys Lys Phe 475 480 485			1612
35	TAC TCC TTT GAG AAG TAC TGG TGT AAG TGG AGC AAC AGA GGC TGC AGC Tyr Ser Phe Glu Lys Tyr Trp Cys Lys Trp Ser Asn Arg Gly Cys Ser 490 495 500			1660
40	GCC CTG CCC ACC CAG AAC GAC GGC CCC AGC CAG GCC TTT GTG AGC TGC Ala Leu Pro Thr Gln Asn Asp Gly Pro Ser Gln Ala Phe Val Ser Cys 505 510 515			1708
45	GAC CAG AAC AGC CAG GTC GTC TCC CTG AAC CTG GAC ACA GTC ACC AAG Asp Gln Asn Ser Gln Val Ser Leu Asn Leu Asp Thr Val Thr Lys 520 525 530 535			1756
50	GAG GAT GAA GGC TGG TAC TGG TGT GGA GTG AAG GAA GGC CCC CGA TAC Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Pro Arg Tyr 540 545 550			1804
55	GGG GAG ACG GCG GCT GTC TAC GTG GCA GTG GAG AGC AGG GTG AAG GGG Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu Ser Arg Val Lys Gly 555 560 565			1852
60	TCC CAA GGC GCC AAG CAA GTG AAA GCT GCC CCT GCG GGG GCG GCA ATA Ser Gln Gly Ala Lys Gln Val Lys Ala Ala Pro Ala Gly Ala Ala Ile 570 575 580			1900
65	CAG TCG AGG GCC GGG GAG ATC CAG AAC AAA GCC CTT CTG GAC CCC AGC Gln Ser Arg Ala Gly Glu Ile Gln Asn Lys Ala Leu Leu Asp Pro Ser 585 590 595			1948
70	TTT TTC GCA AAG GAA AGT GTG AAG GAC GCT GCT GGT GGA CCC GGA GCA Phe Phe Ala Lys Glu Ser Val Lys Asp Ala Ala Gly Gly Pro Gly Ala 600 605 610 615			1996
75	CCT GCA GAT CCT GGC CGC CCT ACA GGA TAC AGC GGG AGC TCC AAA GCA Pro Ala Asp Pro Gly Arg Pro Thr Gly Tyr Ser Gly Ser Ser Lys Ala 620 625 630			2044
80	CTG GTC TCC ACC CTG GTG CCC CTG GCC CTG GTC CTG GTC GCA GGG GTC Leu Val Ser Thr Leu Val Pro Leu Ala Leu Val Leu Val Ala Gly Val 635 640 645			2092

	GTG GCG ATC GGG GTG GTC CGA GCC CGG CAC AGG AAG AAC GTC GAC CGG	2140
	Val Ala Ile Gly Val Val Arg Ala Arg His Arg Lys Asn Val Asp Arg	
	650 655 660	
5	ATT TCA ATC AGG AGC TAC CGG ACA GAT ATC AGC ATG TCA GAC TTT GAG	2188
	Ile Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu	
	665 670 675	
10	AAC TCC AGG GAT TTT GAA GGA CGT GAC AAC ATG GGA GCC TCT CCA GAG	2236
	Asn Ser Arg Asp Phe Glu Gly Arg Asp Asn Met Gly Ala Ser Pro Glu	
	680 685 690 695	
15	GCC CAA GAG ACG TCT CTC GGA GGG AAG GAC GAG TTT GCC ACC ACT ACC	2284
	Ala Gln Glu Thr Ser Leu Gly Gly Lys Asp Glu Phe Ala Thr Thr	
	700 705 710	
20	GAG GAC ACC GTG GAG AGC AAA GAA CCC AAG AAG GCA AAG AGG TCG TCC	2332
	Glu Asp Thr Val Glu Ser Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser	
	715 720 725	
25	AAG GAG GAA GCC GAC GAG GCC TTC ACC ACC TTC CTC CTC CAG GCC AAA	2380
	Lys Glu Glu Ala Asp Glu Ala Phe Thr Thr Phe Leu Leu Gln Ala Lys	
	730 735 740	
30	AAC CTG GCC TCC GCC GCA ACC CAG AAC GGC CCG ACA GAA GCC TAG ACGGAG	2431
	Asn Leu Ala Ser Ala Ala Thr Gln Asn Gly Pro Thr Glu Ala	
	745 750 755	
35	CCCTGGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAATCACGC TGATCCTCAG	2491
	GGCCCTCAGC TCGGGGGGCT CCACTGCCTG CACTCACACC CCGCCTAGGC TTCTCCTGTC	2551
	TGTCCTCAGA GGGTGTGCTG GTTCCCTCTT GGTGGCATCC AAGCCTGGCT TACTTGTTC	2611
40	TATTGGGGGT GAGGTGGTAC GAGGAGTTCC CACCTGCAGC TTATTGGAAC GAGAGAACTA	2671
	AAGGTGTGGA GGAGAATTAA GATCGCAGAG GGGCCTCTCA GAAAGAAAAG GAGTGGGTGG	2731
	GGAGACAACC GCAGAAAGGG GGCCATTGAG CGCTTCCCTG TCCCCTTATT TGGGGATGTC	2791
45	AGTGGAAATCC TCCCTCCAC CCCATCTCTG CACCTCTCCA TCCCCACTCC ATTCCATCTT	2851
	CTCTTCTTCT TTCCCTCATT AAAATGTGC ATTTGGTTAC TCACTAGATT CCAGGGACTC	2911
50	TGCTAGACAC TGGGATAGGT AGGCCGCAAT CCCAGGCGGC AGCCTTCCGC AAACATCAAG	2971
	GAGCCCTGG AGCCACAGC ATCTCTTCAC GTGTACACTC ACTGACCTCT GCCTCTGCTG	3031
	GGAGAAATCA TAAAGGTCT GCAGCCCTGA GGCCTTAGGG ATTATGTAAC ACAGGCATAC	3091
55	ACACAAGGCA CCATCAACAC ATTCTTACCA TTTCACAGGT GAGAAAGCCG AGGTCCTGAG	3151
	AGGTGGAGAG GTTTGCTCAG AGTCAGCAAG TGAGATGTAC GAGTCTCAAG CTAAAGATTT	3211
	GACACCTGCT GTCCCTACAG GAGGGCCTCC TCTCTCCAGA TGAGACAGCA TTCCATAGGA	3271
60	AGGAGAAGAA AAATGTAAAT AAGACTGGTC TTTCACAGGC CCCACATCAG GGAAGATACC	3331
	CCTTCCCTG TCTGTCACTC ACAGAGACCT AATAGGATAA GAGAATGGTC AACACTCAAA	3391
	CCCCGAATG TGAAGAGTTC TAAGTGAAA GGGAGGAAAA AGGGGGGATT TGATGGTGCC	3451
	AGGGAGGGGC TGATCTCCAA AGAACTAAGG TTTAAGTTTT TTTGTTTTTT TTTTCTCTC	3511
65	TTCTAAGCTC TGCACTTCAA CTAGCATCTA TGAGCTGGCA CTTGCTAACA AATCAAAAAAT	3571

GTGAATTAAT TAATAATTAA AGACCATGAT TTCCTCCAAA AAAAAAAAAA AAAAAAAAAA 3630

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 757 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Arg Leu Phe Leu Ala Cys Leu Leu Ala Ile Phe Pro Val Val  
 1 5 10 15  
 20 Ser Met Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Ser Ser Val Glu  
 20 25 30  
 Gly Arg Ser Val Ser Ile Lys Cys Tyr Tyr Pro Pro Thr Ser Val Asn  
 35 40 45  
 25 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Gln Gly Arg Cys  
 50 55 60  
 30 Thr Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Asp Asp Tyr Val Gly  
 65 70 75 80  
 Arg Ala Asn Leu Thr Asn Phe Pro Glu Ser Gly Thr Phe Val Val Asp  
 85 90 95  
 35 Ile Ser His Leu Thr His Lys Asp Ser Gly Arg Tyr Lys Cys Gly Leu  
 100 105 110  
 Gly Ile Ser Ser Arg Gly Leu Asn Phe Asp Val Ser Leu Glu Val Ser  
 115 120 125  
 40 Gln Asp Pro Ala Gln Ala Ser His Ala His Val Tyr Thr Ile Asp Leu  
 130 135 140  
 Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Thr Arg Ala Asn Ser Glu  
 145 150 155 160  
 Lys Arg Lys Ser Leu Cys Lys Lys Thr Ile Gln Asp Cys Phe Gln Val  
 165 170 175  
 50 Val Asp Ser Thr Gly Tyr Val Ser Asn Ser Tyr Lys Asp Arg Ala His  
 180 185 190  
 Ile Ser Ile Leu Gly Thr Asn Thr Leu Val Phe Ser Val Val Ile Asn  
 195 200 205  
 55 Arg Val Lys Leu Ser Asp Ala Gly Met Tyr Val Cys Gln Ala Gly Asp  
 210 215 220  
 Asp Ala Lys Ala Asp Lys Ile Asn Ile Asp Leu Gln Val Leu Glu Pro  
 225 230 235 240  
 Glu Pro Glu Leu Val Tyr Gly Asp Leu Arg Ser Ser Val Thr Phe Asp  
 245 250 255  
 65 Cys Ser Leu Gly Pro Glu Val Ala Asn Val Pro Lys Phe Leu Cys Gln  
 260 265 270



Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala  
 625 630 635 640  
 5 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg  
 645 650 655  
 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp  
 660 665 670  
 10 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp  
 675 680 685  
 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys  
 690 695 700  
 15 Asp Glu Phe Ala Thr Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro  
 705 710 715 720  
 20 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr  
 725 730 735  
 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn  
 740 745 750  
 25 Gly Pro Thr Glu Ala  
 755

30

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 3095 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 40 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(ix) FEATURE:

45 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 85....2400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

50 TCACCTGGAG AGAAGGAAGT AGCTAAACA TTCTCATACA AGAAGCCAAC CTGAGCGGCA 60  
 CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG 111  
 Met Arg Leu Tyr Leu Phe Thr Leu Leu  
 1 5  
 55 GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC 159  
 Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro  
 10 15 20 25  
 60 CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC 207  
 Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr  
 30 35 40  
 TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA 255  
 Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg  
 45 50 55

65

	CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC	303
	Gln Gly Ala Ser Gly Met Cys Thr Thr Leu Ile Ser Ser Asn Gly Tyr	
	60 65 70	
5	CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG	351
	Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu	
	75 80 85	
10	AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT	399
	Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr	
	90 95 100 105	
15	GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC	447
	Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe	
	110 115 120	
20	GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC	495
	Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr	
	125 130 135	
25	CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT	543
	His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro	
	140 145 150	
30	TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA	591
	Phe Lys Arg Glu Asn Val Pro Ser Lys Lys Ser Leu Cys Lys Lys Thr	
	155 160 165	
35	AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC	639
	Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro	
	170 175 180 185	
40	AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGC ACC GAC CTA ACT	687
	Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr	
	190 195 200	
45	GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGC CTG	735
	Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu	
	205 210 215	
50	TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT	783
	Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val	
	220 225 230	
55	GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG	831
	Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu	
	235 240 245	
60	AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC	879
	Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn	
	250 255 260 265	
65	GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC	927
	Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile	
	270 275 280	
70	ATT AAC ACC CTG GGC AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG	975
	Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu	
	285 290 295	
75	ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC	1023
	Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly	
	300 305 310	
80	CTG AGG AAG GAG GAT GCA GGC CAC TAC CAG TGT GGA GCC CAC AGT TCT	1071
	Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser	

	315	320	325	
5	GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val 330 335 340 345			1119
10	AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC Asn Glu Glu Ser Thr Ile Pro Asn Arg Arg Ser Val Val Lys Gly Val 350 355 360			1167
15	ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser 365 370 375			1215
20	AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His 380 385 390			1263
25	TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu 395 400 405			1311
30	GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val 410 415 420 425			1359
35	ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu 430 435 440			1407
40	ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala 445 450 455			1455
45	GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr 460 465 470			1503
50	GCA GTA CTA GGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys 475 480 485			1551
55	TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Ser Ser Asn Lys Gly Cys 490 495 500 505			1599
60	CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser 510 515 520			1647
65	TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser 525 530 535			1695
70	AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr 540 545 550			1743
75	TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg 555 560 565			1791
80	GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val 570 575 580 585			1839

	GCT	CTG	GAA	GAA	GAG	GTA	GTG	GAC	TCC	TCC	ATC	AGT	AAA	GAG	AAc		1887
	Ala	Leu	Glu	Glu	Glu	Val	Val	Asp	Ser	Ser	Ile	Ser	Glu	Lys	Glu	Asn	
					590					595					600		
5	AAA	GCC	ATT	CCA	AAT	CCC	GGG	CCT	TTT	GCC	AAC	GAA	AGA	GAG	ATA	CAG	1935
	Lys	Ala	Ile	Pro	Asn	Pro	Gly	Pro	Phe	Ala	Asn	Glu	Arg	Glu	Ile	Gln	
				605					610					615			
10	AAT	GTG	AGA	GAC	CAA	GCT	CAG	GAG	AAC	AGA	GCA	TCT	GGG	GAT	GCT	GGC	1983
	Asn	Val	Arg	Asp	Gln	Ala	Gln	Glu	Asn	Arg	Ala	Ser	Gly	Asp	Ala	Gly	
				620				625					630				
15	AGT	GCT	GAT	GGA	CAA	AGC	AGG	AGC	TCC	AGC	TCC	AAA	GTG	CTG	TTC	TCC	2031
	Ser	Ala	Asp	Gly	Gln	Ser	Arg	Ser	Ser	Ser	Ser	Lys	Val	Leu	Phe	Ser	
				635			640					645					
20	ACC	CTG	GTG	CCC	CTG	GGT	CTG	GTG	CTG	GCA	GTG	GGT	GCT	ATA	GCT	GTG	2079
	Thr	Leu	Val	Pro	Leu	Gly	Leu	Val	Leu	Ala	Val	Gly	Ala	Ile	Ala	Val	
						655					660					665	
	TGG	GTG	GCC	AGA	GTC	CGA	CAT	CGG	AAG	AAT	GTA	GAC	CGC	ATG	TCA	ATC	2127
	Trp	Val	Ala	Arg	Val	Arg	His	Arg	Lys	Asn	Val	Asp	Arg	Met	Ser	Ile	
					670					675					680		
25	AGC	AGC	TAC	AGG	ACA	GAC	ATT	AGC	ATG	GCA	GAC	TTC	AAG	AAC	TCC	AGA	2175
	Ser	Ser	Tyr	Arg	Thr	Asp	Ile	Ser	Met	Ala	Asp	Phe	Lys	Asn	Ser	Arg	
				685					690					695			
30	GAT	TTG	GGA	GGC	AAT	GAC	AAC	ATG	GGG	GCC	TCT	CCA	GAC	ACA	CAG	CAA	2223
	Asp	Leu	Gly	Gly	Asn	Asp	Asn	Met	Gly	Ala	Ser	Pro	Asp	Thr	Gln	Gln	
				700				705					710				
35	ACA	GTC	ATC	GAA	GGA	AAA	GAT	GAA	ATC	GTG	ACT	ACC	ACG	GAG	TGC	ACC	2271
	Thr	Val	Ile	Glu	Gly	Lys	Asp	Glu	Ile	Val	Thr	Thr	Thr	Glu	Cys	Thr	
				715			720					725					
40	GCT	GAG	CCA	GAA	GAA	TCC	AAG	AAA	GCA	AAA	AGG	TCA	TCC	AAG	GAG	GAA	2319
	Ala	Glu	Pro	Glu	Glu	Ser	Lys	Lys	Ala	Lys	Arg	Ser	Ser	Lys	Glu	Glu	
						735					740				745		
	GCT	GAC	ATG	GCC	TAC	TCG	GCA	TTC	CTG	CTT	CAG	TCC	AGC	ACC	ATA	GCT	2367
	Ala	Asp	Met	Ala	Tyr	Ser	Ala	Phe	Leu	Leu	Gln	Ser	Ser	Thr	Ile	Ala	
					750					755					760		
45	GCA	CAG	GTG	CAC	GAT	GGT	CCC	CAG	GAA	GCC	TAG	GCAGTGCTGA	CCACCCACCC				2420
	Ala	Gln	Val	His	Asp	Gly	Pro	Gln	Glu	Ala							
				765				770									
50	TTGCCTGTGA	CAATCAACTT	GAGAATCACA	CTGATCCGCT	CGCAGCCCAC	ACTCACCCAT											2480
	CACCTCCGCT	CTTCCCTCCT	GTCCTCAGAG	GTGTGCTGGT	TCCTTCCTCG	GCCATGGAAG											2540
	CCTGGCCTAG	TTACGCCTGT	TTAGGAGAGA	GTGTGAGGCG	TTCTTTTCTC	TATGAAGAGA											2600
55	GTGAGGTGGA	AATGAGGAGG	AGGTGAACCT	GAGAGACATC	TCTGGAGGAA	GAGGGTTGAG											2660
	AATAGGGGCT	CGTTTCAGGA	GAAAAGGCCA	TTTGAATCTT	CTTTATAACC	ATATGATAGG											2720
	ATGTCAGCGT	AACTCTTCTC	TCCTCCATCT	CTCCTTTCCT	ATCCTCTTGA	TTCAAACAAC											2780
60	ACATCTGAGA	ACTCACTAGG	CTTCAGTGCC	TACTAAATGC	TGAGAGCCAG	GCCACAATCT											2840
	TTCTATAAAT	ATTACTGGAA	GAGATGCCAT	CTCCTCCCAG	ATTCTGTCTT	TTCATTAAGA											2900
65	TAAGACATCA	TTACCAGGCA	TACCTCCTGC	CTCTGTGCCT	CATAGGCATA	CACAAGCCAT											2960



AAGGGCATCA TGATTTTCAG ATGAGAAGAG ATGTTTCTCA AGAGTGCCTA GTGAGATAGA 3020  
 CTAGCGTCAA ACCAGATGTG GCAACTCCTG GCTCTTGGCC TACGATCTGT CTTCAAGAAA 3080  
 5 AAAAAAAAAA AAAAA 3095

(2) INFORMATION FOR SEQ ID NO: 8:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20 Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val  
 1 5 10 15  
 25 Ser Thr Lys Ser Pro Ile Phe Gly Pro Gln Glu Val Ser Ser Ile Glu  
 20 25 30  
 Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn  
 35 40 45  
 30 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys  
 50 55 60  
 Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly  
 65 70 75 80  
 35 Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn  
 85 90 95  
 Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu  
 100 105 110  
 40 Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser  
 115 120 125  
 45 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile  
 130 135 140  
 Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro  
 145 150 155 160  
 50 Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val  
 165 170 175  
 Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys  
 180 185 190  
 55 Leu Phe Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser  
 195 200 205  
 60 His Leu Thr His Asn Asp Ala Gly Leu Tyr Ile Cys Gln Ala Gly Glu  
 210 215 220  
 Gly Pro Ser Ala Asp Lys Lys Asn Val Asp Leu Gln Val Leu Ala Pro  
 225 230 235 240  
 65 Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu

	245	250	255
	Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg		
5	260	265	270
	Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg		
	275	280	285
10	Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn		
	290	295	300
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly		
	305	310	315
15	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp		
	325	330	335
	Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro		
20	340	345	350
	Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile		
	355	360	365
25	Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys		
	370	375	380
	Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr		
	385	390	395
30	Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp		
	405	410	415
	Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr		
35	420	425	430
	Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp		
	435	440	445
40	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn		
	450	455	460
	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe		
	465	470	475
45	Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr		
	485	490	495
	Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp		
50	500	505	510
	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu		
	515	520	525
55	Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr		
	530	535	540
	Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile		
	545	550	555
60	Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro		
	565	570	575
	Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Glu Val Val		
	580	585	590
65	Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly		

595                      600                      605

Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln  
610                      615                      620

5 Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg  
625                      630                      635                      640

10 Ser Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu  
645                      650                      655

Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His  
660                      665                      670

15 Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile  
675                      680                      685

Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn  
690                      695                      700

20 Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp  
705                      710                      715                      720

Glu Ile Val Thr Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys  
725                      730                      735

25 Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala  
740                      745                      750

30 Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro  
755                      760                      765

Gln Glu Ala  
770

(2) INFORMATION FOR SEQ ID NO: 9:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear  
DESCRIPTION: Rat Polyimmunoglobulin Receptor

(ix) FEATURE:

50 (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 74....2383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 GGCAACGAAG GTACCATGGA TCTTATACAA GAAGTGAACC AACATGCCGC AACCTCCTTG 60  
GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC 109  
Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val  
1 5 10

60 TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG 157  
Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val  
15 20 25

65 AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC 205  
Ser Ser Ile Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp

	30	35	40	
5	ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA CAA GGA GCC Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala 45 50 55 60	253		
10	AAC GGC TAC TGC GCA ACC CTC ATC TCT TCA AAT GGC TAC CTC TCG AAG Asn Gly Tyr Cys Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys 65 70 75	301		
15	GAG TAT TCA GGC AGA GCC AGC CTC ATC AAC TTC CCA GAG AAT AGC ACA Glu Tyr Ser Gly Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr 80 85 90	349		
20	TTT GTG ATT AAC ATT GCA CAT CTC ACC CAG GAG GAC ACT GGG AGC TAC Phe Val Ile Asn Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr 95 100 105	397		
25	AAG TGT GGT CTG GGT ACC ACT AAC CGA GGC CTG TTT TTC GAT GTC AGC Lys Cys Gly Leu Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser 110 115 120	445		
30	CTG GAG GTC AGC CAG GTT CCT GAG TTC CCA AAT GAC ACC CAT GTC TAC Leu Glu Val Ser Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr 125 130 135 140	493		
35	ACA AAG GAC ATA GGC AGA ACT GTG ACC ATC GAA TGC CGT TTC AAA GAG Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu 145 150 155	541		
40	GGG AAT GCT CAT AGC AAG AAA TCC CTG TGT AAG AAG AGA GGA GAG GCC Gly Asn Ala His Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala 160 165 170	589		
45	TGC GAA GTT GTC ATC GAC TCT ACT GAG TAC GTG GAC CCC AGC TAT AAG Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys 175 180 185	637		
50	GAC AGA GCA ATC CTT TTT ATG AAA GGG ACC AGC CGC GAT ATA TTC TAT Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr 190 195 200	685		
55	GTC AAC ATT AGC CAC CTA ATA CCC AGT GAT GCT GGA CTG TAT GTT TGC Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys 205 210 215 220	733		
60	CAA GCT GGA GAA GGC CCC AGT GCT GAT AAA AAT AAT GCT GAC CTC CAG Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln 225 230 235	781		
65	GTG CTA GAG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG AGG TCC TCA Val Leu Glu Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser 240 245 250	829		
70	GTG ACT TTT GAA TGT GAC CTG GGC CGT GAA GTG GCA AAT GAT GCC AAA Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys 255 260 265	877		
75	TAT CTG TGT CGG AAG AAC AAG GAA ACC TGT GAT GTC ATC ATC AAC ACC Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr 270 275 280	925		
80	CTG GGC AAG AGA GAT CCA GCC TTT GAA GGC AGG ATC CTG CTA ACC CCC Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro 285 290 295 300	973		

	AGG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC CTG AGG AAG	1021
	Arg Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys	
	305 310 315	
5	GAG GAT GCA GGG CAC TAC CAG TGT GGA GCG CAC AGT TCT GGT TTG CCT	1069
	Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro	
	320 325 330	
10	CAA GAA GGC TGG CCC GTC CAG GCT TGG CAA CTC TTT GTC AAT GAA GAG	1117
	Gln Glu Gly Trp Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu	
	335 340 345	
15	TCC ACG ATT CCC AAT AGT CGC TCT GTT GTG AAG GGT GTC ACA GGA GGC	1165
	Ser Thr Ile Pro Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly	
	350 355 360	
20	TCT GTG GCC ATC GTC TGT CCC TAT AAC CCC AAG GAA AGC AGC AGC CTC	1213
	Ser Val Ala Ile Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu	
	365 370 375 380	
	AAG TAC TGG TGT CAC TGG GAA GCC GAC GAG AAT GGA CGC TGC CCG GTG	1261
	Lys Tyr Trp Cys His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val	
	385 390 395	
25	CTC GTG GGG ACC CAG GCC CTG GTG CAA GAA GGA TAT GAA GGC CGA CTG	1309
	Leu Val Gly Thr Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu	
	400 405 410	
30	GCA CTG TTC GAT CAG CCG GGC AGT GGC GCC TAC ACT GTC ATC CTC AAC	1357
	Ala Leu Phe Asp Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn	
	415 420 425	
35	CAG CTC ACC ACC CAG GAT TCT GGC TTC TAC TGG TGT CTT ACC GAT GGT	1405
	Gln Leu Thr Thr Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly	
	430 435 440	
40	GAC TCT CGC TGG AGA ACC ACG ATA GAA CTG CAG GTT GCT GAA GCT ACA	1453
	Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr	
	445 450 455 460	
	AAG AAG CCA GAC CTT GAG GTG ACA CCA CAG AAC GCG ACC GCG GTG ATA	1501
	Lys Lys Pro Asp Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile	
	465 470 475	
45	GGA GAG ACC TTC ACA ATC TCC TGC CAC TAT CCG TGC AAA TTC TAC TCC	1549
	Gly Glu Thr Phe Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser	
	480 485 490	
50	CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC GAC GGC TGC CAC ATC CTG	1597
	Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu	
	495 500 505	
55	CCG AGC CAT GAT GAA GGT GCC CGC CAG TCC TCT GTG AGC TGT GAC CAG	1645
	Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln	
	510 515 520	
60	AGC AGC CAG ATC GTC TCC ATG ACC CTG AAC CCG GTC AAA AAG GAA GAT	1693
	Ser Ser Gln Ile Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp	
	525 530 535 540	
	GAA GGC TGG TAC TGG TGT GGG GTA AAA GAA GGT CAG GTC TAT GGA GAA	1741
	Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu	
	545 550 555	
65	ACT ACA GCC ATC TAT GTA GCA GTT GAA GAG AGG ACC AGA GGG TCA CCC	1789
	Thr Thr Ala Ile Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro	

	560	565	570	
5	CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu 575 580 585	1837		
10	GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn 590 595 600	1885		
15	CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly 605 610 615 620	1933		
20	GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly 625 630 635	1981		
25	GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu 640 645 650	2029		
30	GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val 655 660 665	2077		
35	CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr 670 675 680	2125		
40	GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GCC AAT Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn 685 690 695 700	2173		
45	GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly 705 710 715	2221		
50	AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu 720 725 730	2269		
55	TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr 735 740 745	2317		
60	TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp 750 755 760	2365		
65	GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT Gly Pro Gln Glu Ala 765	2422		
	TGAGAATCAC ATTGATCCAC TCGCAGCCCA CCCTCGCCCA TCACCCAGGC TCTTCCCTCC	2482		
	TGTTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG	2542		
	TTTAGGAGAG AGCGTGAGGA GTTCTTTTTC CTGTTAAAGA GTAAGGTGGA AATGAGTTGA	2602		
	GCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTT AGGAGGAAGA	2662		
	GCCATTTGAA GCCTCTTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT	2722		
	CTCTCCTTTC TTCTCTTCTT GATTGAGACA ACAGATCCGA AAACCTACTA GGCTTCCGGT	2782		

GTCTACTAAA TGCTGAGAGT CAGGCCACAG CCTTTCTATA AACATCACTG GAAGAGACAC 2842  
CACCTCGTCC CAGATTCTGT CTTTTCCCTA AGCTATCAAT CATTACCGGG GATTCCCTTT 2902  
5 GCCTCTGCAC CTCATAGGCA ACAAAGAAA CATAAGTCCT GCAGTCTAAG GCATACCCAA 2962  
GCCATAAGGG CACCACGAGA CTCAGATGAG AAGAGATTTT TCTCCAGAGT ACTCAGTGAG 3022  
10 ATAGACTAGT GTCAAGCCAG ATGGGGCAAC TCCTGGCTCT TGGCCTGGGA CTTGTCTTCA 3082  
AGATCTCTGC TCTTATTAGA GAAAGAACTT TAGCATGAGG AAAAGTAAGA GAAAACAAGT 3142  
TACATGGGCA TGGTGGTGTG CTCCTGCAAT CCCAATATTA AGAGGTAAAG AAATAGGACC 3202  
15 AGAAGTTTAA AGTAATCCTT GGCTACCTAG TGAGTGTAAAG GCCAGCCTGG AATCAATAAG 3262  
AGTTGGT 3269

20

(2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 770 amino acids  
(B) TYPE: amino acid  
(C) STRANDNESS: single  
(D) TOPOLOGY: linear  
30 DESCRIPTION: Rat Polyimmunoglobulin Receptor

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val  
1 5 10 15  
35 Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu  
20 25 30  
40 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn  
35 40 45  
Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys  
50 55 60  
45 Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly  
65 70 75 80  
Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn  
85 90 95  
50 Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu  
100 105 110  
Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser  
115 120 125  
55 Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile  
130 135 140  
60 Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His  
145 150 155 160  
Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val  
165 170 175  
65 Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile

	180	185	190
	Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser		
	195	200	205
5	His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu		
	210	215	220
10	Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro		
	225	230	235
	Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu		
	245	250	255
15	Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg		
	260	265	270
	Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg		
	275	280	285
20	Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn		
	290	295	300
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly		
	305	310	315
25	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp		
	325	330	335
30	Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro		
	340	345	350
	Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile		
	355	360	365
35	Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys		
	370	375	380
40	His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val Leu Val Gly Thr		
	385	390	395
	Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu Ala Leu Phe Asp		
	405	410	415
45	Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr		
	420	425	430
	Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly Asp Ser Arg Trp		
	435	440	445
50	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Lys Lys Pro Asp		
	450	455	460
55	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile Gly Glu Thr Phe		
	465	470	475
	Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr		
	485	490	495
60	Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu Pro Ser His Asp		
	500	505	510
65	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Ile		
	515	520	525



Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr  
 530 535 540  
 5 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile  
 545 550 555 560  
 Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro  
 565 570 575  
 10 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Glu Ala Met  
 580 585 590  
 Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg  
 595 600 605  
 15 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln  
 610 615 620  
 Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly  
 625 630 635 640  
 Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu  
 645 650 655  
 25 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys  
 660 665 670  
 Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met  
 675 680 685  
 30 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly  
 690 695 700  
 Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile  
 705 710 715 720  
 Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala  
 725 730 735  
 40 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu  
 740 745 750  
 Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu  
 755 760 765  
 45 Ala

50 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Guy's 13 Kappa

60 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 8....320

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTCGAGC GAC ATT GTG ATG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT 49  
 Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser  
 1 5 10

5 CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT GCC AGC TCA AGT GTA AGT 97  
 Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser  
 15 20 25 30

10 TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC ACT TCT CCC AAA CTC TGG 145  
 Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp  
 35 40 45

15 CTT TAT AGC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT 193  
 Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser  
 50 55 60

20 GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC CGA ATG GAG 241  
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu  
 65 70 75

GCT GAA GAT GCT GCC ACT TAT TAC TGC CAT CAA AGG ACT AGT TAC CCG 289  
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro  
 80 85 90

25 TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA A TA 322  
 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
 95 100 105

30 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 105 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Guy's 13 Kappa

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly  
 1 5 10 15

45 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr  
 35 40 45

50 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 50 55 60

55 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu  
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr  
 85 90 95

60 Phe Gly Gly Gly Thr Lys Leu Glu Ile  
 100 105

65 (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Guy's 13 Gamma 1

## 10 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 7...402

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCGAG	ATG	GAA	TGG	ACC	TGG	GTT	TTT	CTC	TTC	CTC	CTG	TCA	GGA	ACT	48	
	Met	Glu	Trp	Thr	Trp	Val	Phe	Leu	Phe	Leu	Ser	Gly	Thr			
1					5							10				
GCA	GGC	GTC	CAC	TCT	GGG	GTC	CAG	CTT	CAG	CAG	TCA	GGA	CCT	GAC	CTG	96
Ala	Gly	Val	His	Ser	Gly	Val	Gln	Leu	Gln	Ser	Gly	Pro	Asp	Leu		
15					20					25				30		
GTG	AAA	CCT	GGG	GCC	TCA	GTG	AAG	ATA	TCC	TGC	AAG	GCT	TCT	GGA	TAC	144
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	
				35				40						45		
ACA	TTC	ACT	GAC	TAC	AAC	ATA	CAC	TGG	GTG	AAG	CAG	AGC	CGT	GGA	AAG	192
Thr	Phe	Thr	Asp	Tyr	Asn	Ile	His	Trp	Val	Lys	Gln	Ser	Arg	Gly	Lys	
			50					55						60		
AGC	CTT	GAG	TGG	ATT	GGA	TAT	ATT	TAT	CCT	TAC	AAT	GGT	AAT	ACT	TAC	240
Ser	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Asn	Thr	Tyr	
		65					70					75				
TAC	AAC	CAG	AAG	TTC	AAG	AAC	AAG	GCC	ACA	TTG	ACT	GTA	GAC	AAT	TCC	288
Tyr	Asn	Gln	Lys	Phe	Lys	Asn	Lys	Ala	Thr	Leu	Thr	Val	Asp	Asn	Ser	
	80						85					90				
TCC	ACC	TCA	GCC	TAC	ATG	GAG	CTC	CGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	336
Ser	Thr	Ser	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	
95					100					105				110		
GCA	GTC	TAT	TAC	TGT	GCA	ACC	TAC	TTT	GAC	TAC	TGG	GGC	CAA	GGC	ACC	384
Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	
				115					120					125		
ACT	CTC	ACA	GTC	TCC	TCA											402
Thr	Leu	Thr	Val	Ser	Ser											
				130												

## 55 (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 132 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear  
 DESCRIPTION: Guy's 13 Gamma 1

## 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

30

35

40

45

ACCAGATCTA TGGGAATGGAC CTGGGTTTTT C 31

55

60

CCCAAGCTTG GTTTTGGAGA TGGTTTCTC 30

65

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATAAGCTTG GTCCTACTCC TCCTCCTCCT A 31

15

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATCTCGACT CAGTAGCAGA TGCCATCTCC 30

30

## 35 (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGAAAGCTTT GTACATATGC AAGGCTTACA 30